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The Spatial Extent Contaminants and the Landscape Scale: An Analysis of the Wildlife, Conservation Biology, and Population Modeling Literature

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1 **The Spatial Extent of Contaminants and the**
2 **Landscape Scale: An Analysis of the Wildlife,**
3 **Conservation Biology and Population Modeling Literature**

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7
8 **Abstract**

9 Many contaminant releases to the terrestrial environment are of small areal extent. However,
10 rather than evaluating the ecological impact on species in the immediate vicinity of the release, it
11 may be more ecologically meaningful to determine if population impacts occur at the landscape
12 level. In order to do this, the cumulative impact of all releases in the landscape under
13 consideration must be evaluated. If the release sites are viewed as localized areas that are no
14 longer available for use by ecological receptors (that is, no longer part of the habitat), this can be
15 thought of as a modified form of habitat fragmentation. In most studies, habitat fragmentation is
16 viewed as the loss of large areas of habitat within a landscape, leaving small isolated patches of
17 intact habitat within a hostile matrix. Small-scale contaminant releases, on the other hand,
18 results in small areas of hostile (i.e., unavailable) matrix within a primarily intact habitat. With
19 this consideration in mind, we analyzed the wildlife and conservation biology literature to
20 determine if information on habitat size requirements such as home range or critical patch size
21 could inform us about the potential for impact at the landscape level from release sites based on
22 the size of the release alone. We determined that evaluating the impact of release size had to be
23 conducted within a contextual basis (considering the existing state of the landscape). Therefore,

1 we also reviewed the population modeling literature to determine if models could be developed
2 to further evaluate the impact of the spatial extent of chemical releases on the landscape. We
3 identified individual-based models linked to geographic information systems to have the greatest
4 potential in investigating the role of release size with respect to population impacts at the
5 landscape level.

6
7 **Keywords:** ecological risk assessment; home range; critical patch size; population models;
8 fragmentation; oil spills; brine spills; exploration and production sites; Tallgrass Prairie Preserve;
9 ecological screening tools

10 **Introduction**

11 The need for the use of ecological risk assessments (ERAs) to evaluate the potential impacts
12 of chemical releases on ecological receptors has been well recognized since the early 1990's
13 [1,2]. Much of the early development work on ERAs was based on the human health risk
14 assessment paradigm as laid out in 1983 within the National Research Council's "Red Book" [3].
15 The United States Environmental Protection Agency (EPA) expanded upon the Red Book
16 concept to develop guidance for conducting ERAs [4]. Many states followed suit with similar
17 guidance [5]. Even at this early date the guidance was explicit that populations, communities,
18 and ecosystem function were the endpoints to be protected (except for the case of threatened and
19 endangered species). However, most ERAs conducted at terrestrial sites consisted of estimated
20 exposure to individual members of a species potentially found at a site [6]. The selected species
21 represent site-specific trophic levels, and are those species most likely to be exposed to the
22 contaminant. To make the calculations more tractable, individuals of the species are often
23 assumed to reside in the area of contamination 100% of the time. Exposure pathways are

1 identified, and the resulting exposures are estimated. The exposure estimate is then divided by a
2 critical endpoint (usually derived from the literature), resulting in the calculation of a Hazard
3 Quotient (HQ). Hazard Quotients greater than 1 suggest the potential for adverse ecological
4 impact.

5 Although such HQ-based ERAs are still commonly conducted in screening level ERAs [7], it
6 has become increasingly recognized that estimating potential impact to individuals of a species
7 does not necessarily translate to population-level impacts at larger, more ecologically-relevant
8 spatial scales. The need to consider impacts at more relevant spatial scales is specifically called
9 out in more recent USEPA guidance documents [8, 70], but these documents do not describe
10 how to consider such impacts, although several case studies for watersheds are available [9].

11 **The Issue of Space**

12 In terrestrial systems, chemical releases are typically of small areal extent, as small as a few
13 hundred square meters, and usually not larger than a few hectares [10,11]. Many of these small
14 spills are gas stations, dry cleaners, and other sites within an urban setting with few significant
15 ecological resources [12]. However, there are many sites owned by the Department of Defense,
16 the Department of Energy, the oil and gas and other industries that contain large intact ecological
17 landscapes with minimal development. Chemical releases at these sites tend to be small and
18 localized within the context of a larger landscape. In addition, many of the types of releases
19 involve chemicals that do not persist or bioaccumulate to any significant extent. This suggests
20 that ecological impacts resulting from these spills would be felt primarily in the immediate
21 vicinity of the spill.

22 The impact of such localized spills can be thought of as a type of habitat depletion or
23 degradation. A petroleum or solvent release may locally degrade or make uninhabitable portions

1 of the landscape. Emergency response actions may involve the physical removal of
2 contaminated soil, resulting in a bare, initially uninhabited area. Some releases, such as water of
3 extremely high salinity produced during oil production can result in scars on the landscape that
4 remain devoid of vegetation for many years. Figure 1 shows examples of such releases.

5 Such removal of habitat from the landscape can be thought of as a form of habitat
6 fragmentation. Habitat fragmentation contains three components 1) loss of habitat, 2) reduction
7 in habitat patch size, and 3) increased isolation of habitat patches [13] (Figure 2a). However, the
8 “fragmentation” resulting from chemical releases is much more limited in extent (Figure 2b). In
9 addition, there is also the potential for some ecological recovery from the releases, returning the
10 release site to some level of ecological function.

11 Such habitat loss needs to be considered from a larger spatial scale than the local area of the
12 release. When one first considers the impact to populations from a landscape scale, it may seem
13 obvious that such small releases will be unlikely to result in population-level impacts. For
14 example, although soil invertebrates and small mammals inhabiting the release site may suffer
15 direct mortality, populations of these species over the entire landscape may show little overall
16 impact [68]. Indeed, many states are developing exclusion criteria based on the size of release
17 using just this logic [14, 69]. However, there is a limit to the amount of habitat loss a population
18 can endure before severe impacts are observed and there becomes a threat of extirpation of a
19 population from the landscape. In addition, the distribution of multiple small spills across the
20 landscape may have consequences beyond just that attributable to cumulative loss of habitat.
21 Dispersal and metapopulation dynamics could potentially be impacted [15, 46, 65–67], resulting
22 in reduced fecundity and ultimately population size.

1 There is a large and varied literature from the wildlife, ecology and conservation biology
2 fields on the spatial requirements of individuals and populations of various species. This
3 literature has focused on the impacts of fragmentation on a variety of species. In addition, there
4 is a large literature on modeling a population's use of the landscape. Therefore, we undertook an
5 analysis of the literature to 1) summarize data on species home range and critical patch size
6 requirements and determine if these data could assist us in evaluating how the removal of habitat
7 resulting from a chemical spill could impact a species use of space and 2) review the population
8 models that are available and determine their usefulness in assessing the impact of habitat loss
9 due to chemical spills. Most practitioners of ecological risk assessments have training in
10 toxicology versus wildlife biology or population modeling. Therefore, the intent of this analysis
11 and review is to introduce the ERA practitioner to the available literature on home range size,
12 critical patch size, and population modeling that may be useful in expanding how ERAs are
13 currently conducted.

14 **The Home Range and Critical Patch Size Literature**

15 We conducted an extensive search of the literature by reviewing 31 databases containing
16 over 31.9 million records. This included an extensive search within the conservation biology
17 literature. It also covered environmental literature external to this specific field in an effort to
18 fully capture any research related to species home range and critical patch size. We developed
19 two keyword or "concept" lists to direct the search. The search strategy involved a full scan of
20 each record and selection of those records that included one concept from each of two concept
21 lists. Concepts with multiple words required that each word occur within 3-5 words of the other.
22 We excluded any records that specifically and wholly studied insects. Records that included

1 insect data in addition to higher-level species data did receive full concept matching and/or
2 subsequent review.

3 This refined search produced approximately 3,000 potentially relevant records. A review of
4 these abstracts further refined the number of full articles ordered and reviewed to approximately
5 300 articles. Finally, we perused each article to identify useful data. This effort involved
6 specifically defined objectives that guided the manner in which we constructed the conceptual
7 literature search strategy and final review techniques. We collected data for several parameters
8 including fragmentation sensitivity, foraging distance, and dispersal range and we noted this data
9 in the article review. However, we focused on delineating empirical home range and critical
10 patch sizes for a wide range of species, both in our initial literature search and the subsequent
11 article perusal. Appendices of tables summarizing the literature review protocol, the data
12 extracted from the review, and relevant citations are available from the authors upon request or at
13 <http://www-erd.llnl.gov/library/>.

14 In examining these articles, we removed any research articles containing data derived
15 through modeling. We compiled only empirical data in order to potentially construct coarse
16 screening tools to use in evaluating chemical spill release sizes. Empirical data potentially have
17 a higher utility in developing these tools in that they represent field data that more fully accounts
18 for environmental variability. Although modeling data are valuable in developing screening
19 tools (as we show later), we initially wanted to identify the quantity and quality of available
20 empirical data for a wide range of species. Given the capacity to build a substantive database
21 from this information, the resultant screening tool may be useful in screening the impact of the
22 size of chemical release sites across landscapes.

1 An intensive review of the relevant articles resulting from the literature search provided a key
2 insight. Identification of data representing home range size proved a fairly straightforward
3 process (although there are multiple methods of determining home range). In contrast, a limited
4 number of research articles used terminology that directly classified their empirically derived
5 data as representing “critical patch size”. Rather, the majority of studies identified their results
6 from a particular field study or experiment using varying definitions.

7 We consequently needed to identify the range of research methods employed that resulted in
8 data useful to measure species’ critical patch size. This better ensured we included all relevant
9 data rather than excluding large quantities of available measures informing our critical patch size
10 database. We found several ways of interpreting this parameter existed. Critical patch size can
11 be interpreted to include:

- 12 The minimum patch size below which the species is never found,
- 13 The minimum patch size below which the species is not present in 100% of the patches,
- 14 The minimum patch size that can sustain a viable population, or
- 15 The percentage of habitat that must be remaining for the species to be found in the
- 16 landscape.

17 If a single article used multiple indirect measures of critical patch size, we selected the value
18 for the minimum patch size below which the species is never found. Typically, an article used
19 only one of the above measures and we made note of the specific one used to provide
20 information that potentially explains differences in critical patch size for a given species across
21 studies. The most commonly used measure tended towards the presence or absence type of
22 study. In summary, the literature review produced a database populated with critical patch data
23 that were either directly or (more likely) indirectly specified.

1 All compiled data for home range size used terminology directly identifying this measure.
2 We used the generally accepted definitions for both home range and critical patch size. We
3 defined home range to be the amount of area required by an individual to successfully survive
4 and reproduce. We defined critical patch size to be that quantity of area required to maintain a
5 population. The scalar difference in definitions should be noted, as this produced a demonstrable
6 contrast in the summary statistics.

7 This extensive literature review resulted in the construction of a substantive database on
8 home range and critical patch size (249 species). However, this database required further
9 refining due to differences in data reporting and conformities needed for statistical analysis.
10 Data points reported as percentage of habitat remaining were not used in calculating the
11 summary statistics. Also, data provided as a range of values (e.g., 2-200 ha) remained in the
12 database but were not used for generating summary statistics. We noted values reported as
13 approximations in the database but used the absolute value for the purposes of calculations (e.g.,
14 575 ha rather than ~575 ha). Similarly, measures given in terms of less or greater than a specific
15 value were noted but used as an absolute data point (e.g., 5,000 ha rather than >5,000 ha). In the
16 case of lower tail truncated data (less than values), use of truncated data is justified as these
17 values represent areas the species could easily persist on or use, although the actual required area
18 may be even smaller. The justification for the use of upper tail truncated data (greater than)
19 values is a bit more problematic. By using the absolute value, we are making the assumption the
20 species could persist on or use this area, where as the actual area may be much larger. However,
21 none of the 162 home range values had upper tail truncated data. Of the 276 critical patch size
22 values, five values were listed as “greater than or equal to” and only one value was listed as
23 “greater than”. Thus any bias introduced through the use of upper tail truncated data should be

1 minimal. Any qualitative data points (e.g., several ha) remained in the database but were
2 considered unsuitable for calculations. Despite this described range of needed data refinements,
3 the actual number of data disregarded for generating summary statistics was less than 10% of the
4 total number of compiled data points.

5 We segregated the species' data into varying taxonomic groups. It is especially important to
6 observe that the resolution of this taxonomic partitioning was much lower for birds than any
7 other taxonomic group. Essentially, one group existed for all birds whereas mammals were more
8 finely divided based on feeding strategies.

9 **Limitations of Home Range and Critical Patch Size Data**

10 A general review of the data pointed to several elements requiring further consideration.
11 This included the fact that methodologies used to quantify home range and critical patch size
12 differed widely. These differing methodologies may substantively impact the results generated.
13 Few standardized methods are agreed upon or used. Our review did not investigate the degree to
14 which this affects any statistics calculated for each individual species or group of species;
15 however, this remains an area for further analysis.

16 Also, few papers examined the species dynamics associated with large areas of intact habitat
17 containing smaller patches of unavailable matrix. Rather, the majority of studies examined the
18 dynamics caused by smaller patches of habitat remaining from a larger landscape system. As a
19 result, the data collected generally represent the species' requirements given the traditional view
20 of fragmentation and the associated environmental context. In the context of fragmentation
21 presented in this paper, empirical studies may find differences in the species' dynamics not
22 captured in the data found from this current literature review. Testing whether the dynamics of

1 this unique fragmentation scenario proves a critical variable in generating species data may
2 represent another area of remaining interest.

3 The data coverage across taxonomic groups varied in terms of home range size. Small and
4 large mammals had a relatively greater range of species with representative data available than
5 any other group. Yet, the number of data points available from the current literature for each
6 individual species proved limited. Table 1 shows that although empirical research tends to focus
7 on mammals, the number of studies per species does not largely differ between taxonomic group.
8 Of the represented species for each group, the median and mean number of data points is simply
9 one to two studies.

10 Critical patch studies were available for a wider range of species in each group (Table 2).
11 With this parameter, birds were the most intensively studied, with the remaining groups
12 essentially studied equally. However, this data again shows the pattern of low numbers of
13 studies on an individual species basis. Both the median and mean number of data points did not
14 exceed two for any species.

15 A wide variation existed in reported home range size for each species, further complicating
16 our analysis. This may be the result of varying methodologies in both gathering data and
17 calculating the home range size. Given that our literature review produced few data points per
18 species, the effect of combining few represented species with a paucity of data points and large
19 variances in reported values will result in highly variable summary statistics. In addition, if
20 some of the representative species populating a group in this database happens to have very
21 small or large size requirements, this will also produce skewed results for the taxonomic groups
22 as a whole.

1 **Calculation of Home Range and Critical Patch Size Summary Statistics**

2 Summary statistics using the refined data compiled from the home range and critical patch
3 size literature were calculated. These summary statistics included the number of data points per
4 species (as discussed above), the range for these values, medians, means, and standard
5 deviations. The mean and median values for the taxonomic groups were similar. For this reason
6 we used the mean values to further assess species size requirements. As shown in Figure 3, the
7 average home range and critical patch size across groups revealed an overall pattern. As the
8 species size associated with a taxonomic group increased, a concurrent increase in size
9 requirements occurred.

10 The exception to this pattern occurred within the bird taxonomic group for home range size
11 and we believe this may be explained by the fact that we placed all birds within one group while
12 giving a finer resolution of taxonomic segregation to other groups of animals. For example, a
13 bird species with a very large home range (e.g., a prairie falcon or boreal owl) was placed in the
14 same group as species requiring much smaller areas (e.g., scarlet tanager). In addition, the
15 literature review resulted in a very limited coverage of birds for home range size. Given such a
16 small number of representative species, and a group populated with some raptors, birds with
17 large home range sizes heavily skewed the value for this parameter towards a large required area.
18 In contrast, we more finely delineated taxonomic differences in mammals, separating small
19 mammals from larger mammals and further differentiating between the food preferences for
20 these large mammals (distinctions such as herbivorous versus carnivorous mammals). As a
21 result, the home range size requirements of a species such as the coyote did not bias the value for
22 the mammal group within which the prairie vole existed. It should be noted that the literature

1 review produced more extensive home range data coverage for mammalian species than other
2 groups. This fact also aids to lessen any bias in its summary statistics.

3 The average critical patch size required by the taxonomic groups (Figure 3) shows this same
4 general pattern without the exception observed for bird home range size. As expected, the
5 overall area requirements increase as one moves from lower to higher taxonomic groups. This
6 result for critical patch size (as compared to that observed for home range) may be due to a more
7 even spread of data throughout the groups. The data populating critical patch size requirements
8 included a wider range of species as well as a relatively greater number of data points per
9 species. Therefore, the bird group did not display the heavily biased nature towards
10 overestimation as displayed in its home range size requirements.

11 Available home range data for herptiles was limited, both in the range of species represented
12 and number of data points for each species. Given that this limited number of represented
13 species and studies produced small values for this parameter, it is likely that home range size is
14 underestimated. Yet, as shown in Figure 3, its required critical patch size probably represents a
15 relatively more accurate estimation due to a fuller species representation providing data for this
16 parameter.

17 Despite these possible data difficulties, an overall pattern is observed, both across and within
18 groups. As previously described, the size requirements of both parameters display a pattern in
19 which increasing area needs occur, on average, as the overall size of the species within each
20 taxonomic group increase. Other species variables may be responsible for this pattern; our
21 review did not attempt to statistically correlate any species variables to our parameters of
22 interest. Rather, we focused on delineating overall patterns in these parameters for the
23 taxonomic groups while constructing a database of individual species area requirements.

1 Within each taxonomic group, critical patch size requirements exceed that of home range for
2 each group with the exception of birds (see above for a possible explanation of this discrepancy).
3 This would be expected given that critical patch size was defined at the population level and
4 home range was defined at the organism level. Although some individual species may require a
5 larger home range size than another species critical patch requirements, the fact the aggregate
6 statistic for multiple species displayed this pattern provides evidence we had an adequate species
7 representation and number of data points per species. Unfortunately, we were unable to locate
8 critical patch size information for large herbivorous mammals.

9 **Using Home Range and Critical Patch Size Data to Evaluate Impacts of Spill Size**

10 To show how home range and critical patch size might be used to conduct a screening level
11 evaluation of the effect of spill size, we use the Tallgrass Prairie Preserve (TPP) to serve as a
12 case study site. The overall habitat in this preserve is largely intact. The site is also an active oil
13 exploration and production site. A legacy of oil and brine releases to the environment has
14 resulted in either the temporary or permanent loss of small but multiple habitat areas within the
15 landscape. Therefore, the TPP represents the type of habitat fragmentation that is the focus of
16 this paper. We have been using the TPP as a case study in our efforts to develop large-scale
17 habitat criteria to conduct ecological risk assessments for landscapes with multiple chemical
18 releases [16, 17].

19 The TPP comprises approximately 15,000 hectares of several habitat types including prairie,
20 savanna, woodland, pasture, and crop (Table 3). Tallgrass prairie represents the major habitat
21 type. The Nature Conservancy manages the preserve. Their management strategy includes
22 restoring natural ecological components and processes (e.g., reintroduction of bison and
23 disturbance regimes such as fire and grazing) to this landscape system [18]. The preserve also

1 supports petroleum production sites. Multiple wells are located within the preserve, both active
2 and inactive. Each well area occupies 55 – 100 m² of area, while the well sites use 2.6 ha in total
3 area. The number of wells with surface features is 337 [19]. The total length of roads within the
4 preserve is 198 km [20] with a total road area of 73 ha. These production sites left a small
5 legacy of brine and oil spills, with each individual spill limited in areal extent. Thus, multiple
6 release sites occur across this landscape and the cumulative impact of these at a landscape scale
7 is not known.

8 We used these area summary statistics for the habitat types to take a first cut at a screening
9 assessment. Figure 4 conceptually demonstrates this broad screening method. This figure
10 compares average home range size for the general taxonomic groups (species not specific to just
11 the TPP), to the TPP habitat areas. With this comparison one can easily assesses if sufficient
12 area of each habitat type is available at the TPP to support the taxonomic groups in general.
13 After excluding the bird group due to its insufficient data mentioned above, all natural habitat
14 types have enough area to support the home range needs of the general taxonomic groups. The
15 pasture and crop habitats do not have enough area to meet the home range size requirements of
16 the large mammals. However, these habitats that are unlikely to be the primary habitat for most
17 of the mammalian species and thus their small area may not be a problem.

18 This pattern changes somewhat when we look at critical patch size requirements (Figure 5).
19 This comparison shows the available area of the habitat types at the TPP do not fully support the
20 critical patch size requirements of all groups. The critical patch size requirements for small and
21 large mammals exceed that generally available in all habitats. Again, although birds and
22 herptiles do not have adequate habitat area in the pasture and crop areas, these habitats probably
23 do not represent their preferred habitat area and therefore may not represent any difficulty for the

1 species. Habitats that provide a quantity of area that well exceeds a taxonomic group's
2 requirements will probably not be at risk for ecological impacts at the population scale when the
3 quantity of aggregate hostile matrix (i.e. spill areas) from releases is removed from this overall
4 landscape.

5 While such a comparison may provide some insight as to the overall ability of the TPP to
6 support many taxonomic groups, an analysis using species actually found at the TPP may prove
7 more useful. Therefore, we reviewed our database for species likely to be present at the TPP. At
8 least one third of the species in our database represented species observed at the TPP [17].
9 However, the study locations for these species varied widely and may not be entirely analogous
10 to this specific landscape.

11 Figure 6 and 7, respectively, compare the average home range and critical patch size
12 requirements of species occurring at the preserve with TPP habitat areas. These comparisons
13 allow us to assess the relationship between specific assessment endpoint species and available
14 habitat area. For home range size, all habitats have enough area to meet these requirements for
15 endpoint species, again with the exception of pasture and crop habitats. As already described,
16 this will only present a problem in the unlikely case that these species solely use these specific
17 habitats to fulfill their home range needs. On the other hand, species critical patch size
18 requirements exceed that available for some habitats, pointing to possible habitat constraints.
19 This may result in potential ecological impacts if the habitat is further fragmented by multiple
20 chemical releases. The large mammal assessment endpoint (i.e., the coyote) barely meets its
21 requirements in even the largest habitat type (the prairie). Assuming that a large amount of this
22 habitat becomes unavailable due to multiple, small chemical releases, this screening analysis
23 suggests a potential impact that may require further detailed analysis. One also needs to include

1 an assessment of habitat use patterns for these species and whether these species specialize in
2 particular habitats or may successfully utilize other areas if pressed.

3 Finally, Figure 8 and Table 4 show the relationship between specific species critical patch
4 size requirements and TPP prairie habitat with the inclusion of the total brine spill area. Here,
5 assuming a non-random distribution of the multiple brine spills (i.e., all occur within the prairie),
6 these spills may result in a substantial portion of necessary habitat being lost or degraded.
7 Obviously, several assumptions are involved in this conclusion, including that the species
8 specialize in using this particular habitat and cannot travel to another more distant prairie habitat
9 outside of the preserve. However, the intent of the screening tool is to indicate a need for further
10 analysis, not conclusively indicate a definitive ecological impact.

11 **The Utility of Home Range and Critical Patch Size Data in Developing Size Screening**

12 **Criteria**

13 Our efforts in conducting this literature review and constructing a database of home range
14 and critical patch size requirements aimed to assess whether aggregate values for these
15 parameters may serve as effective, although gross, screening tools for landscapes impacted with
16 multiple releases of small areal extent. The summary statistics do show an interesting overall
17 pattern. However, the number of species populating each taxonomic group is fairly low. Few
18 data points for each species and widely varying measurement techniques limit the usefulness of
19 the aggregate statistics. There are additional limitations with the critical patch size data. While
20 we found substantially more data for this parameter, there continued to be limited species
21 representation, inadequate quantities of data points for each species, and a large range in reported
22 values. This disparity in reported values is probably the result of using four methods for
23 indirectly measuring this parameter. This limits the usefulness of aggregating the data.

1 It may be more meaningful to evaluate home range and critical patch size data on a site-
2 specific basis. For example, given a particular site, one could determine home range and critical
3 patch size requirements for taxonomic groups specific to the site. Again, the strength of this
4 evaluation depends on data availability. The larger the breadth of species representation and the
5 number of replicate studies using similar measurement methodologies, the stronger the analysis.

6 Alternatively, one may consider individual species requirements. For example, in a given
7 landscape, a particular trophic chain comprised of identified endpoint species may be used to
8 grossly evaluate the impact of spill size. One may compare the home range and critical patch
9 size requirements of these species against the remaining area of available habitat (essentially, the
10 landscape with the release site areas removed). Such a screening tool may provide usefulness as
11 an indicator that either initiates more detailed assessments and modeling or allows for an exit
12 strategy.

13 Thus, currently the best use of home range and critical patch size data appears to be at the
14 individual species level for a specific site. In order to make a more meaningful general
15 conclusion, conducting an evaluation of many sites with their specific species and comparing
16 home range and critical patch size data to spill areas, and aggregating these results could prove
17 useful. However, such a crude evaluation does not take into account the effect of the spatial
18 distribution of spills across the landscape, and the possible impact on populations levels through
19 its impact on migration and dispersal. Modeling is a useful means of evaluating the implications
20 of both spill size and distribution. It could be used to evaluate any gross size criteria developed
21 through the home range and critical patch size evaluation by modeling effects on multiple
22 species in multiple habitat types, with changes in number, size and distribution of spills across
23 the landscape.

1 **Application of Population Models to Habitat Loss from Chemical Spills**

2 The problem of the effect of habitat loss on animal populations has been reviewed frequently
3 [13, 21–23]. Andren [21] points out that natural processes, such as fire and windfall, fragment
4 habitats, but that the largest factor causing habitat fragmentation is human land use. We can
5 categorize the models, which are used to study habitat loss, by their level of organization or the
6 scale of the processes considered explicitly. In particular, most models, which have been used
7 to study habitat loss, belong to one of three model classes, which we review here:
8 metapopulation, demographic, and foraging. These three classes of models cover a wide range
9 of model assumptions and at least three levels of organization. We will not review pure
10 movement models, which operate only at very short time scales and do not include effects at the
11 population level. For each model type, we will review temporal and spatial scales as well as
12 results that evaluate the effects of habitat loss. We will particularly focus on the ability of each
13 model type to evaluate the impacts of habitat loss of small aerial extent of various distributions
14 across the landscape, such as the type expected in the case of chemical spills in a terrestrial
15 environment.

16 In the sequence meta-population models, demographic models, and foraging models, the
17 modeled processes and the spatial resolution are both increasingly detailed (Table 5). Spatial
18 ecological attributes, such as home range or critical patch size, are treated very differently in the
19 different model types.

20 **Metapopulation Models**

21 Levins [24, 25] developed metapopulation theory from the theory of island biogeography of
22 MacArthur and Wilson [26]. Levins posits that any large population (a metapopulation)
23 comprises a set of local subpopulations residing on their respective patches in the environment

1 [27]. Simplistically, a metapopulation is a population of populations. Any of the local
 2 populations can become extinct within a time interval, creating an empty patch for
 3 recolonization. The metapopulation is maintained by recolonization of the empty patches.

4 *Spatially-Implicit Metapopulation Models*

5 To see how the spatial scale affects results, consider two types of metapopulation models,
 6 spatially-implicit and spatially-explicit. First, consider the spatially implicit case [28, 29] in
 7 which a fraction h of the total area of patches is usable. Let p be the fraction of occupied
 8 patches. Assume that all occupied patches can re-colonize all empty patches. The differential
 9 equation for the change in p is

10
$$\frac{dp}{dt} = cp(h - p) - ep \tag{1}$$

11 where c and e are the parameters for the colonization and the extinction rate, respectively (Fig.
 12 9). Note that in metapopulation models, the internal dynamics of a local population is ignored.
 13 All demographic processes are subsumed into the extinction rate, ep . The colonization rate is
 14 proportional to the product of occupied patches p and suitable unoccupied patches $(h-p)$. At
 15 steady state, the fraction of occupied patches is

16
$$p^* = h - \frac{e}{c}, \tag{2}$$

17 and the fraction of suitable unoccupied patches is

18
$$h - p^* = \frac{e}{c} \tag{3}$$

19 First, note that e must be less than c for these equations to make sense. Secondly, note that as
 20 suitable habitat falls from $h=1$ to $h_c=e/c$, the occupied patches decrease from a maximum $p^* =$
 21 $(1-e/c)$ to $p^*=0$ (or extinction), respectively. Thirdly, note that the fraction of unoccupied
 22 patches is fixed at a constant value of e/c if h is greater than e/c . As h decreases from e/c down

1 to zero, occupied habitat is zero and unoccupied habitat decreases from e/c to zero (Fig. 10a).
 2 These considerations lead to the astonishing result that if we remove any patches such that the
 3 fraction of patches removed equals the current number that are occupied ($h-e/c$) leaving a total
 4 fractional amount of suitable habitat of e/c , then the species will go extinct. Lawton et al. [30]
 5 and Doncaster et al. [31] point out that the "extinction threshold", $h_c=e/c$, is analogous to the
 6 "eradication threshold" in epidemiology. That is, it is unnecessary to inoculate everyone
 7 (remove habitat) to drive a pathogen to extinction. Rather, in both cases there is a particular
 8 amount of habitat, which if removed will cause extinction.

9 Nee and May [32] generalized the one-species case discussed above to two competitive
 10 species (1 and 2) with two equations for their respective fractions of occupied patches of p_1 and
 11 p_2

$$12 \quad \frac{dp_1}{dt} = c_1 p_1 (h - p_1 - p_2) - e_1 p_1 + c_1 p_1 p_2 \quad (4)$$

13 and

$$14 \quad \frac{dp_2}{dt} = c_2 p_2 (h - p_1 - p_2) - e_2 p_2 - c_1 p_1 p_2 \quad (5)$$

15 These equations imply that both species 1 and 2 can invade the empty patches, and species 1
 16 (the superior competitor) can invade all patches occupied by species 2. At steady state for both
 17 competitors to exist ($p_1 > 0, p_2 > 0$), eqs. 4 and 5 imply that $h > e_1/c_1 > e_2/c_2$. Thus there must be a
 18 sufficiency of suitable habitat and the weaker competitor (species 2) must either have a lower
 19 extinction rate or a more efficient (larger) colonization rate (or both) than the superior
 20 competitor. These equations imply that the extinction threshold for species 1, the better
 21 competitor, is $h_{c1}=e_1/c_1$. At this value of h , the weaker competitor (stronger disperser) reaches a

1 peak occupation rate of $p_{2,\max}=e_1/c_1 - e_2/c_2$. For h less than e_1/c_1 , p_2 falls linearly, reaching 0 at
 2 $h_{c_2}=e_2/c_2$. For h between e_2/c_2 and e_1/c_1 , the fraction of unoccupied sites is constant with a
 3 value of e_2/c_2 . For h between 1 and e_1/c_1 , the inferior competitor (superior disperser) increases
 4 in abundance as h decreases and the superior competitor decreases in abundance (Figure 10b).
 5 Thus Nee and May point out that habitat destruction can favor “weedy” species.

6 These results have obvious implications when evaluating the removal of patches from a
 7 habitat as a consequence of chemical spills. Multiple spills could exceed the number of occupied
 8 patches of species with small home range requirements, ultimately driving a species to
 9 extinction.

10 *Spatially-Explicit Metapopulation Models*

11 Moilanen and Hanski [33] and Hanski [34], using the incidence model (Fig. 11) of Hanski
 12 [35], found that the results of Nee and May [32] can be altered profoundly when one considers
 13 explicitly the spatial arrangement of habitat undergoing habitat loss. For the one-species case, let
 14 J_i be the probability that the species occurs on patch i . Let C_i be the probability of colonization
 15 at the end of a time-step conditioned on non-occupation at the beginning of the time-step. Let E_i
 16 be the probability of extinction at the end of the time-step conditioned on occupation at the
 17 beginning of the time-step. At steady state, the probability of extinction ($J_i E_i$) is balanced by the
 18 probability of colonization [$C_i(1-J_i)$] and the probability of *rescue* during the time-step ($J_i E_i C_i$)

19 or

20
$$J_i = \frac{C_i}{C_i + E_i - E_i C_i} \tag{6}$$

1 Hanski [35] assumes

$$2 \quad E_i = \frac{m}{A_i^x} \quad (7)$$

3 and $C_i = M_i^2 / (M_i^2 + y^2)$ where $M_i = \prod_{j \neq i}^n p_j \exp(-\beta d_{ij}) A_j$, A_j is the area of patch j , d_{ij} is the inter-
4 patch distance between patch i and patch j , n is the number of patches, $p_j=1$ if patch j is occupied
5 and $p_j=0$ otherwise, and m , x , y , β , and β are model parameters. These parameters are fixed from
6 field observations.

7 Moilanen and Hanski [33] constructed a two-species simulator for this model, which
8 followed the rule that the superior competitor could always invade (instantaneously replace) the
9 inferior competitor. The inferior competitor had a smaller value of β (better disperser). They
10 simulated four cases: 1) a real network of 96 habitat patches for Glanville Fritillary (*Melitaea*
11 *cinxia*), 2) a hypothetical 200-patch network of log normally-distributed sizes and random
12 placement, 3) case 2 with colonization from a mainland, and 4) case 2 with the patches crowded
13 or aggregated together rather than randomly placed. Recall that in the Nee and May [32]
14 calculation, the extinction point for the superior competitor is fixed at $h_{c1}=e_1/c_1$. Moilanen and
15 Hanski [33] found that the extinction points for the superior competitor in cases 1, 2, 3, and 4
16 were $h_c=0.6, 0.5, 0.0$, and 0.2 , respectively. Furthermore, the qualitative shape of the frequency
17 distribution for both species and for the unoccupied patches was different between the four
18 different cases. In all four cases, as the fraction of available habitat decreases from 1 to 0, the
19 empty habitat rises to peaks at $h_{high,max}=0.65, 0.75, 0.7$, and 0.3 , respectively. As h continues to
20 decrease, the empty habitat falls to a minimum at $h_{min}=0.45, 0.5, 0.4$, and 0.2 , respectively. For

1 h below this point, as h decreases, the frequency of empty patches rises to another smaller, local
2 maximum at $h_{low,max}=0.35, 0.2, 0.2,$ and $0.1,$ respectively, before falling to zero at $h=0$. In
3 contrast, Nee and May [32] found that the empty habitat fell linearly from a maximum at $h=1$
4 until the superior competitor went extinct at $h_{c1}=e_1/c_1$. Below that value of h , Nee and May [32]
5 found that the empty patch frequency stays constant until the weaker competitor goes extinct.
6 Thus Nee and May [32] did not find two peaks separated by a minimum as was found by
7 Moilanen and Hanski [33] in the spatially explicit case. Furthermore, the positions of the
8 maxima and minimum in the spatially–explicit case depend strongly on the physical arrangement
9 of the patches.

10 Introducing a spatial resolution, in which patches are explicit, produces a profound difference
11 in model results compared to the spatially implicit calculation. This clearly has implications
12 when considering the distribution of spills across a landscape. These results reinforce the need
13 for site-specific assessments when evaluating the impacts of chemical-related spills.

14 **Demographic Models**

15 Metapopulation models were implemented at the population level of organization using only
16 one state variable per species (frequency of occurrence of a local population) and two processes,
17 extinction and colonization. The next levels of refinement are the demographic models (Fig. 12),
18 which have the processes of birth, death, stage transitions, settlement, and dispersal. These
19 models allow one to study the interaction of demography with dispersal and habitat structure.
20 These models have state variables of either aggregated numbers in each local population or data
21 records for each individual in the population. The former method is the older approach in
22 population biology [36-39] and the latter approach is the recent, individual-based approach [40].

1 *Temporal Scale and Organization Level*

2 Note that the processes used in demographics models (e.g., reproduction, life-stage
3 transitions, mortality) occur at sub-generational time-scales whereas the extinction process
4 considered in metapopulation models occurs over multi-generational time-scales. Furthermore,
5 demographic models produce results that describe the life-stage distribution within a population
6 whereas metapopulation models only describe presence or absence. The time-scale and the
7 population itself is more finely resolved in demographics models than in metapopulation models.

8 *Consequences of Habitat Loss*

9 Demographic models have been used to study the effects of habitat loss on demography and
10 dispersal. Venier and Fahrig [41] and Fahrig [23, 42] developed a model of demography and
11 dispersal for a theoretical population in a habitat undergoing habitat loss and fragmentation. One
12 external variable controls total breeding habitat and another variable controls aggregation
13 (contagion or clumpiness) of the habitat patches. They found that the variable controlling
14 absolute habitat amount was much more important in determining extinction than the variable
15 controlling patch clumpiness or fragmentation.

16 Kokko and Sutherland [43] examine the consequences for habitat loss if individuals use
17 *floating* strategies in selecting breeding habitat. *Floating* is the decision not to settle and breed
18 even when capable. If there is a range of habitat quality, each individual must decide between
19 occupying a site of a given quality, which will be used for the duration of one's life, and floating
20 with the expectation that a better site will be available later. The authors find that floating affects
21 the consequences of habitat loss. If high quality habitat is removed, the floating population loses
22 members disproportionately compared to the breeding population, because the breeding
23 population supplies the surplus, which is the floating population. If low quality habitat is

1 removed first, there is no effect until habitat is removed at the threshold of use. At that point the
2 breeding population loses members faster than the floating population. One aspect of this
3 problem is that if the high-quality habitat is removed, performing a census of the breeding
4 population will not catch the marked decline of the floating population, which is an important
5 reserve for recovery from other disturbance. The results of Kokko and Sutherland [43] suggest
6 that the value of habitat be explicitly considered in assessments of effects of chemical spills.
7 Such assessments should address the floating population as well as the breeding population.

8 Schneider and Yodzis [44] developed an individual-based model of American marten
9 (*Martes americana*) for application for central Ontario. The model includes both demographic
10 and environmental stochasticity. Deterministic extinction occurs if mortality rate exceeds a
11 critical threshold, such that the population growth rate (PGR) is negative. Probabilistic
12 extinction occurs if PGR is positive but available habitat is low. In these cases, abrupt transitions
13 from survival to extinction are observed as habitat decreases. Also, probabilistic extinction
14 occurs if the PGR is near zero. However, in this case, instead of an abrupt transition, the
15 probability of extinction gradually increases as population size decreases.

16 Letcher et al. [45] developed an individual-based model for the endangered red-cockaded
17 woodpecker (*Picoides borealis*) in mature pine forests in the southeastern U.S. Letcher et al.
18 [45] found that large population sizes had high probability of persistence and low population
19 sizes had high probability of extinction. Persistence and extinction in intermediate size
20 populations were sensitive to spatial arrangement. For this size range, increasing distances
21 between territories significantly lowers the probability of survival.

22 Henein et al. [46] developed a spatially-explicit, individual-based model for two woodland
23 small mammals, the eastern chipmunk (*Tamias striatus*) and the white-footed mouse

1 (*Peromyscus leucopus*). Chipmunks are specialists that prefer wooded habitat and avoid fields of
2 crops. The mice are generalists, which include both forests and grain fields in their habitat.
3 Henein et al. [46] found that chipmunk persistence increased with increasing connectivity in the
4 landscape (increasing fence-rows) and increasing total wooded habitat. The mice population
5 persisted in all simulations for both habitats (wooded and crop). Mice traveled through grain
6 fields as well as along fence rows and so all habitats were well connected. Results are shown in
7 Fig. 13. The mice had larger populations and higher densities than did the chipmunks in
8 identical landscapes. Thus, behavioral characteristics affect the spatial use of resources, which
9 can profoundly affect population size and extinction probability.

10 Rushton et al. [47] developed an individual-based, spatially-explicit model for the
11 population dynamics of water vole (*Arvicola terrestris*), under pressure of both predation by
12 American mink (*Mustela vison*) and habitat fragmentation. The authors found that increasing
13 habitat size significantly lowered the probability of extinction. Including mink predation in the
14 model increased the probability of extinction by about 0.4 for fixed habitat size. Without mink
15 predation, the two most important parameters were brood size and home range requirement,
16 which were negatively and positively correlated, respectively, with extinction probability. With
17 mink predation, the two most important parameters were the level of mink predation and the
18 minimum home range requirement. This suggests that demographics are controlled by brood
19 size and mink predation, and dispersal is controlled by the home range requirement.

20 In demographic models, habitat loss affects dispersal and settlement directly. However,
21 there is no direct dependence of the demographic processes of offspring production, life-stage
22 transition, and mortality on habitat loss. At best, this dependence is treated phenomenologically.
23 The relation between demographic processes and habitat loss may be modeled as empirical

1 functions of such environmental variables as “habitat quality” or by using the “carrying
2 capacity” parameter. Dependence on such parameters implies that baseline population
3 measurements are required to use these models to assess impacts of chemical spills.

4 **Foraging Models**

5 There are many types of foraging models and various aspects have been reviewed elsewhere
6 [48-51]. Depletion of the prey or food resource has been studied both with theoretical models
7 [52] and with pragmatic models [53, 54].

8 For purposes of this paper, we will consider a subset of foraging models that we shall
9 designate as foraging-population models. This subset is the class of population models which
10 simulate all the activities, including foraging, of an entire population during at least one seasonal
11 phase in its life-cycle in which foraging is a critical behavior (Fig.14). These models do not
12 necessarily simulate the entire life cycle or an entire calendar year. In some instances, a
13 foraging-population model may include the entire life cycle including all demographic processes.
14 Foraging-population models often include energetic considerations to evaluate the benefits of
15 acquiring food relative to the metabolic costs necessary for survival.

16 Foraging-population models include processes that operate at sub-life-stage time scales.
17 Realistic simulations of these processes at these shorter time-scales force a spatial resolution
18 more detailed than demographic models. So the progression of models in the sequence
19 metapopulation, demographic, and foraging-population represent a progression of increasing
20 temporal and spatial resolution. Foraging-population models are often implemented as
21 individual-based models to accommodate the details of animal movement and all the interactions
22 between population members and prey (food resource).

1 *Implications of Foraging-Population Models for Spatial Use*

2 Sutherland and Dolman [55] developed a theoretical model to explore the consequences of
3 habitat use on populations obeying Evolutionarily Stable Strategies (ESS). The model includes
4 resource depletion, migration, and density-dependent processes, such as interference between
5 individuals during foraging. The authors studied migration between seasonal breeding patches
6 and winter patches where mortality occurs. Migration costs a food requirement. At each time-
7 step, food intake is calculated and if it falls below a certain threshold, that phenotype dies. This
8 process is repeated until the intake rate of all survivors exceeds the threshold for survival. The
9 ESS emerges over time (multiple generations); at ESS, all individuals in each phenotype have
10 exactly the same intake rate. Loss of wintering habitat produces crowding, raising resource
11 depletion, and interference which in turn lowers intake rates. Lower intake rates lead to
12 increased mortality and lower population levels. These perturbations require time to equilibrate.
13 Habitat loss on a patch reduces the size of the sub-population using that patch. The migrating
14 populations are redistributed among the remaining patches. If habitat is removed piecemeal with
15 the least desirable pieces removed first, the total population decreases slowly at first until it
16 finally crashes when the most desirable patches are finally removed. If the desirable patches are
17 removed first, then dramatic drops in population show up immediately.

18 South [56] discusses a spatially-explicit, individual-based model for female red squirrels
19 (*Sciurus vulgaris*) in a Scots pine (*Pinus sylvestris*) plantation. Foragers gain knowledge as they
20 move over the landscape and this knowledge is used in decision making. South found that home
21 range areas and home range overlap increased with decreasing food density. For constant food
22 density, as range area increases, so does range overlap. South suggests that changes in range
23 area for a constant food density results from depletion competition. Mean range area was more

1 highly correlated with food density than that of mean range overlap. Food density, energy
2 content of the cones, energy cost of staying in the nest, and energy cost of activity were the four
3 most important parameters affecting mean range area. Food density, length of a time step, time
4 to assess cell food value, and the number of nests were the four most important parameters
5 affecting mean range overlap. Notice space-time parameters affect range overlap and energy
6 parameters affect range area. Food density belongs to both categories. Field data showed larger
7 mean range areas than model predictions, but field values for the coefficient of variation in range
8 area agreed with model projections.

9 Carter and Finn [57] constructed an individual-based, spatially explicit model for red
10 foxes (*Vulpes vulpes*) preying on dabbling duck nests. A rule-based expert system determines
11 the current state of the animal and its environment and then supplies an action to the animal to
12 take at each decision point. Results of the expert system model were compared to those of a
13 random model. Home ranges were an emergent property of the model's rules and agreed with
14 the upper bounds of field estimates. The expert system produced movement patterns similar to
15 that observed in the field, including movement in new small areas and movement along borders.
16 The expert system model showed behavior that was not found in the random model.

17 Wolff [58] developed an individual-based model for wood stork (*Mycteria americana*), in the
18 Florida Everglades. He constructed a comprehensive set of rules that govern all aspects of the
19 birds' behavior. Fleming et al. [59] used this model to study the effects of habitat loss on the
20 wood stork population. The Everglades are characterized by sheet flows of water that inundate
21 all land. Low-lying land has a long period between drying (sloughs or long hydroperiod
22 wetlands), while higher land (peripheral wetlands or short hydroperiod wetlands) have a short
23 period between drying. Dry land is used for nesting. Increased upstream water use has affected

1 the Everglades water levels and the drying-reflooding period. Some authorities have suggested
2 that the increased frequency of increased dry period length may have led to reduced levels of fish
3 (food resource) in the Everglades. When short-hydroperiod wetlands are reduced, Fleming et al.
4 [59] observe mass starvation when the habitat loss is greater than a critical point. Short-
5 hydroperiod habitat loss delays nest initiation and shifts some nesting to the long-hydroperiod
6 lands. Likewise a critical point is observed for reductions in long hydroperiod lands. If long
7 hydroperiod habitat is reduced to an amount smaller than the population-size dependent
8 threshold, large population losses occur because of the reduction of the food supply late in the
9 dry season. Results are shown in Fig. 15.

10 *Types of Bottlenecks*

11 Fleming et al. [59] introduce two terms to describe the effect of the losses of short-
12 hydroperiod habitat (peripheral wetlands) and long-hydroperiod habitat (central sloughs). They
13 refer to the former circumstance as a *habitat bottleneck* and the latter as a *resource bottleneck*.
14 “Habitat bottleneck” indicates there is a limited number of sites suitable for nesting. “Resource
15 bottleneck” indicates that the food supply has become limiting. We submit that these notions are
16 useful to categorize the response of populations to habitat loss.

17 *Effect of Habitat Loss on Demographics*

18 The work of Fleming et al. [59] make clear that the effect of habitat loss on demographic
19 processes in foraging-population models can be modeled mechanistically. That is, habitat loss
20 can lead to a decline in feeding rates, which translates into starvation and increased mortality.
21 This linkage is made through the process of foraging and its implication on the energetics of the
22 individual. Thus the effect of habitat loss on demographic processes arises naturally in foraging-

1 population models in a mechanistic manner rather being imposed in an *ad hoc*,
2 phenomenological manner as in demographics models.

3 **Scale, Level of Organization, Home Range, and Critical Patch Size**

4 If we change the level of organization and the concomitant scale at which we view a
5 population, the role of home range and critical patch size also changes. Recall that in
6 metapopulation models, the state variable is frequency of occurrence of a local population. Thus
7 the notion of home range is not meaningful in this context. However, the minimum patch size A_c
8 at which a population is observed to occur (critical patch size) does have meaning and is equal to

$$9 \quad A_c = m^{lx} \quad (8)$$

10 from eq. 7. Thus the critical patch size sets the dependence of the local extinction rate on patch
11 area in the spatially-explicit model of Hanski [34]. However at this scale, one cannot predict
12 sizes of critical areas, either home range or critical patch size.

13 For demographic models implemented with the individual-based approach, we saw that home
14 range was a very important model parameter [47]. Home range can be used to set bin size in
15 relatively low-resolution models or territory requirements in models constructed with finer
16 scales. Demographic models can predict critical habitat size (total size of all habitat for
17 interacting populations) [60–63]. Demographic models can predict critical patch size for very
18 isolated populations, but home range is not predictable at this scale of resolution. Instead, home
19 range for the individual is set, at least in part, by energy requirements, the foraging process, and
20 the food resource.

21 Home range takes on a new significance in foraging-population models. Both South [56] and
22 Carter and Finn [57] found that home range was an emergent property. That is, predicted home
23 range – calculated from movement rules, observed resource densities, and animal energetics –

1 agreed well with observations. By *emergent property*, we mean the quantitative prediction of a
2 new phenomenon at a higher level of organization or larger spatial scale from processes and
3 structures at a lower level of organization or smaller spatial scale. Also, we suggest that critical
4 patch size is predictable by foraging-population models. Critical patch size should be
5 determined by population demographics as modified by behavioral movement rules, availability
6 of resources, foraging success, and energetic requirements.

7 **The Utility of Models in Evaluating the Impact of Spill Size and Distribution**

8 Spatial models are useful in evaluating the implications of chemical spills. The
9 metapopulation models are best used to investigate the potential, gross implications of removal
10 of habitat patches as affected by spill size and distribution. Results from these models may
11 suggest a need to evaluate in more detail specific species and taxonomic groups to determine the
12 actual pattern of response.

13 Individually-based models, whether they be the demographic or foraging-population models
14 described above, have the ability to investigate species responses to various stressors in great
15 detail. However, they are often time-intensive to construct and parameterize. But their great
16 utility in conducting “what if” simulations strongly argue for their use. Such models could be
17 used to investigate the implications of size criteria suggested by the coarser scale evaluation of
18 home range and critical patch size. By simulating different species from different taxonomic
19 groups in different habitats, it may be possible to converge upon a “*de-minimus*” size criteria.
20 These models could also be modified to not only investigate the total loss of habitat due to
21 chemical spills (a pretty severe assumption), but the degradation of habitat. Toxicological
22 effects could be incorporated either phenomenologically (i.e. through impacts on demographic
23 transitions of birth, death, survival, etc), or mechanistically. Population models to investigate the

1 implications of spatial scale are starting to be used in ERAs, for example, the USEPA's PATCH
2 model [64]. Developing a "*de-minimus*" size criterion through an initially intensive use of such
3 population models would be a valuable exercise. Individual-based models are being used to
4 investigate habitat loss from hydrocarbon and brine spills at the Tallgrass Prairie Preserve in
5 Northern Oklahoma [68]. A *de-minimus* size criterion is one of the goals of this project. A *de-*
6 *minimus* size criterion would then limit the use of these complex models to sites where more
7 detailed investigation is truly warranted.

8 **Summary**

9 In this paper, we explored two methods to evaluate the ecological implications of spill size
10 and distribution, 1) comparing home range and critical patch size requirements to total spill size,
11 and 2) conducting population modeling to investigate impacts on demography, migration and
12 dispersal. These two methods lie on opposite ends of the complexity spectrum. The simple
13 comparison of home range and/or critical patch size to spill size is a useful initial evaluation of
14 spill size impact. However, to effectively conduct such an evaluation, it is necessary to know the
15 composite amount of habitat in the landscape containing the spills. By doing this comparison,
16 we can avoid a problem with the blind use of a *de-minimus* size criteria, that is, screening out a
17 small spill that may have impacted the only small, remaining habitat in a more developed area.

18 On the other end of the spectrum we looked at detailed, individual-based models that can be
19 used to explore subtle changes in foraging, dispersal and migration. These models can be used to
20 assist in the development of *de-minimus* size criteria. However, we feel such *de-minimus* size
21 criteria should not be used blindly. Some knowledge of the landscape within which the spill has
22 occurred is essential, and the use of home range and/or critical patch size data in conjunction
23 with *de-minimus* levels may provide the necessary level of protection.

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1 **Table 1:** Number of studies providing home range size data for each species within each guild.

GUILD	Total number of Species	Number of studies per species			
		Min	Max	Median	Mean
Small Mammals	34	1	10	1	1.9
Large Mammals	28	1	12	1	2.5
Birds	8	1	5	2	2
Herptiles	4	1	3	1	1.5

2

3 **Table 2:** Number of studies providing critical patch size data for each species within each
4 guild.

GUILD	Total number of Species	Number of studies per species			
		Min	Max	Median	Mean
Small Mammals	33	1	2	1	1.2
Large Mammals	36	1	4	1	1.2
Birds	77	1	4	1	1.3
Herptiles	44	1	4	2	1.6

5

1 **Table 3:** Habitat types and areas, Tallgrass Prairie Preserve^a.

Habitat	Area (ha)
Woodland	1,866
Savanna	1,919
Prairie	11,198
Pasture	153
Crop	5
Other	4

2 ^aGIS vegetation layers provided by the Oklahoma GAP Analysis Program, Oklahoma State
 3 University, and subsequently analyzed using Arc Info.

4
 5

6 **Table 4:** Brine spill data, Tallgrass Prairie Preserve^a.

Description	Spill Data
Total number of sites with brine damage	126
Total brine spill area	17.4 ha
Median brine spill area	0.02 ha
Range of brine spill area	7 m ² –5 ha
Largest singular brine spill area	5 ha

7 ^a Data collected through aerial photograph analysis by Bryan Tapp,
 8 University of Tulsa, OK, USA